

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 07:25:40 : Search time 727.75 seconds
 (without alignments) 2735.846 Million cell updates/sec

Title: US-09-227-881-1
 Perfect score: 5300
 Sequence: 1 atctttgttcgtttaactc.....caggcacctctacgacagc 5300

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq 36:*

1: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1980.DAT:*

2: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1981.DAT:*

3: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1982.DAT:*

4: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1983.DAT:*

5: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1984.DAT:*

6: /cgtn2_2/gcdata/geneseq/geneseq/NA1985.DAT:*

7: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1987.DAT:*

8: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1988.DAT:*

9: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1989.DAT:*

10: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1990.DAT:*

11: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1991.DAT:*

12: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1992.DAT:*

13: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1993.DAT:*

14: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1994.DAT:*

15: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1995.DAT:*

16: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1996.DAT:*

17: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1997.DAT:*

18: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1998.DAT:*

19: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA1999.DAT:*

20: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA2000.DAT:*

21: /cgtn2_2/gcdata/geneseq/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
1	5299	100.0	5299	19	V51361		Human TIGR promoter
2	5298.4	100.0	5300	19	V51362		Human TIGR promoter
3	5298.4	100.0	5300	19	V51363		Human TIGR promoter
4	5298.4	100.0	5300	19	V51365		Human TIGR promoter
5	5298.4	100.0	5300	19	V51366		Human TIGR promoter
6	5298.4	100.0	5300	19	V51367		Human TIGR promoter
7	5286	99.5	5304	19	V51368		Human TIGR promoter
8	5275.4	99.5	6169	19	V51369		Human TIGR upstream
9	1859	35.1	2800	21	237968		Human GLC1A gene e
c	10	176.4	3.3	283	15	063886	AP2 sequence obcd.
c	11	175.2	3.3	16450	21	062967	Retinoblastoma bin
c	12	174.2	3.3	282	18	T62346	Consensus Alu repe

RESULT 1
 V51361 ID V51361 standard; DNA: 5299 BP.
 XX AC
 XX V51361;
 XX 27-OCT-1998 (first entry)
 XX DE Human TIGR promoter region DNA.
 XX KW TIGR; trabecular meshwork induced glucocorticoid response protein; human;
 XX diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.
 XX Homo sapiens.
 OS PN W09832850-A1.
 XX PD 30-JUL-1998.
 XX PF 09-JAN-1998; 98WO-US00468.
 XX PR 26-SEP-1997; 97US-0938669.
 PR 28-JAN-1997; 97US-0791154.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Chen H, Chen P, Nguyen TD, Polansky JR;
 XX DR WPI; 1998-427946/36.
 XX Use of TIGR nucleic acid sequences - used for, e.g. developing
 PT products for diagnosis, prognosis and treatment of glaucoma
 XX
 PS Claim 34; Fig 1; 105pp; English.
 XX

Query Match 3.3%; Score 175.2; DB 21; Length 162450;
 Best Local Similarity 78.4%; Pred. No. 4.1e-30;
 Matches 210; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

RESULT 11
 ID 286967/c
 ID 286967 standard; DNA; 162450 BP.
 AC AC
 XX XX
 DT 16-MAY-2000 (first entry)
 DE Retinoblastoma binding protein-7 genomic DNA sequence.
 KW RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation; diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis; benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia; lymphoma; ds.
 KW Lymphoma; ds.
 XX OS Homo sapiens.
 XX PN WO20000607-A1.
 XX PD 06-JAN-2000.
 XX PF 30-JUN-1999; 99WO-1B01242.
 XX PR 30-JUN-1998; 98US-0091315.
 XX PR 10-DEC-1998; 98US-0111909.
 XX PA (GEST) GENSET.
 XX PT Bougueret L;
 XX DR WPI; 2000-117170/10.
 PT Novel nucleic acid and polymorphic markers used for diagnosis of diseases, especially those involving abnormal cell proliferation and differentiation -
 PT
 PS Claim 1: Page 118-163; 223pp; English.
 XX CC This sequence represents the retinoblastoma binding protein-7 (RBP-7) genomic sequence of the invention. The RBP-7 coding sequence and regulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and probes derived from the RBP-7 nucleotide sequence (e.g., 287035-287099) are useful for DNA amplification and detection methods. RBP-7 biallelic markers (see 28593-287034) are useful for diagnosis of disease related to alteration in the regulation or in the coding regions of the RBP-7 gene and for prognosis/diagnosis of an eventual treatment with therapeutic agents, especially agents acting on pathologies involving abnormal cell proliferation and/or differentiation, these include thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers, including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, prostate cancer, various leukaemias, and lymphomas. RBP-7 antibodies are useful as diagnostic agents.
 XX Sequence 162450 BP; 45465 A; 3061 C; 32637 G; 53673 T; 14 other; SQ

RESULT 12
 ID T62346/c
 ID T62346 standard; DNA; 282 BP.
 AC AC
 XX T62346;
 XX DT 11-JUN-1997 (first entry)
 DE Consensus Alu repeat sequence.
 KW Bubble; interspersed repetitive element; ligation; annealing; primer; PCR; polymerase chain reaction; amplification; chromosomal aberration; genetic disorder; ss.
 XX OS Homo sapiens.
 XX FH key Location/Qualifiers
 FT primer_bind 22..45
 FT /*tag= "a
 FT /note= "binds primer 47-23 (T62347)"
 FT primer_bind 216..236
 FT /*tag= "b
 FT /note= "binds either primer Alu-S (T62348) or Alu-J (T62349)"
 FT primer_bind 263..282
 FT /*tag= "C
 FT /note= "binds primer Alu-end (T62350)"
 XX PN US5597694-A.
 XX PR 07-OCT-1993; 93US-0133629.
 XX PR 07-OCT-1993; 93US-0133629.
 XX PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Housman DE, Monroe DJ;
 XX DR WPI; 1997-108321/10.
 XX PT Amplification of nucleic acid having interspersed repetitive element - using bubble oligo:nucleotide
 XX PS Disclosure; Column 19-20; 16pp; English.
 XX CC The invention relates to the amplification of region of DNA containing interspersed repetitive elements (IRE) such as the Alu repeat sequence presented here. The method involves ligating a double stranded DNA structure with a non-complementary region, a 'bubble', in the

amplified by the primer pair R14B264/0560mak (T42806-7). The primers also simultaneously amplify the loci 0900 (T42808) and 0120 (T42805). The primers can be used for gene mapping, to assess paternity, maternity and identity of children or in forensic science. In particular, they can be used for the DNA fingerprinting identification of genetically related or unrelated individuals.

Query Match: Best Local Similarity 3.3%; Score 172.8; DB 17; Length 452; Best Match 200; Conservative 1; Members 23; Index 8; Gane 1.

1321 acctgagtcactgtccacccctgcctcccaaggtaaaggaaattccggctcgtccatggcc 1380

b 312 ATCTCAGCTCTACTGCAAACCTCTGCCCTCCAGTTCAAGCGATCTCTTGCCTCAGCCTCC 253

1381	cggtagctggactacaggcg-----gacgccccgttaattttgtatgttga	1432
252	GGATGGCTGGGATTAAGGATGCCGACCTGGCGTAATTGTTGATTTGAGA	193

1433	gatatgggtttcaccaatttttagcccggtgttgcactttaacctccggatcca	1492
b	GAGACGGGGTTTCACCAACGGCTGGCTCAAACTCTGACCTCTGGATCTG	133
192		
1493	cccctctcgactcttaaagtgtctggatcacggatgtacccggccggcc	1543
y		
132	CCGCCTCTCACCTCCAAAGTGCTGGATTCAGGCGATGAGCCACCCGGCC	77

search completed: December 3, 2000, 19:16:21
Job time: 42641 sec

כטבָּה: אֶלְעָזָר בָּרָא

